

FIGURE 1

GGCATCTGCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATCATGCTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTGTTC
CTCCCTTTGCCTGTCAAGATGAATACTGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTGTCATGGAGACTACAGCTTCGAGGCTACCAAGGCCCCCTGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCAAAGGTGAGAAGGGCAGAAAGGTGACCTGGGCCTCGAGGGGAGCAGGG
GCAGCATGGCCCAAAGGAGAGAAGGGCTACCCGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGATTATCTCAGCAGTGTT
GAGACCAACATTGAAACTTCTTGATGTCATGACTGGTAGATTGGGCCCCAGTATCAGG
TGTGTATTCTCACCTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGATGAGGTTGGCTGCAATGGG
CAATGGCGCTCTCCATGGGACCACCAACGCTCTCCACCTTGCAAGGATTCTGCTCTTG
AAACTAAGTAAATATGACTAGAATAGCTCCACTTGGGAAGACTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTACATTGCTGTATTCAAAAATTATT
GGTTGCAATGTTGTCACGCTACAGGTACACCAATAATGTTGGACAATTCAAGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCAGATGACCTGACTAATATACTCAGCATCTTATCAC
TCTTCCTGGCACCTAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTCTAT
CACAGAAGTCATTGCAAAGAATTGACTACTCTGCTTTAATTAAATACCAGTTTCAGG
AACCCCTGAAGTTAAGTTCAATTCTTATAACATTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGCAAGAACAGGGCACTAGCTGCCTTATTAGCTAATTAGTGCCTCCG
TGTTCAGCTTAGCCTTGACCCCTTCTTGTACCCACAAAATACATTAAACTCTGAATT
ACATACAATGCTATTAAAGTCAATAGATTAGCTATAAAAGTGTGCTGACCAGTAATGTGG
TTGTAATTGTTGATGTCACCTTACATGCCCAACTCGGATGTGGGTCAAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTATATCTGAAGAACATACACTATTAATAACCTT
AGAGAAAGATTTGACCTGGCTTAGATAAAACTGTGGCAAGAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTGTAAAGATAAAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686
><subunit 1 of 1, 246 aa, 1 stop
><MW: 26994, pI: 6.43, NX(S/T): 0
MLWRQLIYWQLLALFFLPFCLCQDEYMEPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFSSVETNIGNFFDVTMGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHAVLKLAGDEVWLRMGNGALHGDHQRFSTFAGFLLFETK
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Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: C1q domain signature.

amino acids 137-167

C1q domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGC**ATG**CAGTGAAGCTGGGACCCCTCCTGCTGCCCTGGCT
GGGCCTGGCCCAGCCAGCCTCTGCCGCCGGAAAGCTGCTGGTGTTCGCTGGATGGTTTC
GCTCAGACTACATCAGTGATGAGGCCTGGAGTCATTGCCTGGTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTCCCTAGTCTCTCGTATCCAATTATTA
TACCCTAACATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC
CCACCACCAACAAGTCCTTGACATTGGCGTCAACAAAGACAGCCTAACGCCCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATAAAAA
ATGTCCCAACGGATATCAATTTCGCAATGCACTGCAGCGATGCTCTGACTCCTCAAGAGT
GGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGCCTGCAGGACCGCCTGAACGTCAATTATTCGATCAC
GGAATGACCGACATTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGAGCCTTGGCCGGCCCTGGAAAC
ACTCTGAGATATATAACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTGTCTCCTTGACTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTCCGTTGGATGAACAGCACCGGCA
GGCGGGAAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTATGGACATGCCGGC
ATCTCCTGGCCTTCGGACCTGATTCAAATCCAACCTCAGAGCTGCTCCTATCAGGTCGGT
GGACGTCTACAATGTCAATGTGCAATGTGGTGGCATCACCCGCTGCCAACAACGGATCCT
GGTCCAGGGTGTGCACTGCTGAAGGGCCGCGCCGGACTGCCCGCCTGCTGGCCAGC
CACTGTGCCCTGGCACTGATTCTCTCTTGCCTTGCA**TAA**CTGATCATATTGCTTGTCTC
AGAAAAAAACACCATCAGCAAAGTGGCCTCCAAAGCCAGATGATTTCAATTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCAGTGCACATTGTAAATACATTATTCTGGATAAT
TCTATACATAAAAGTTCTACTTGTAAA

FIGURE 4

MAVKLGTLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTRHCEVHQHMIGNYMWDPTTNKSFDIGVNKDSLMPWWNGSEPLW
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVII FSDHGMDIFW
MDKVIENKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFVSPPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCGCTGCCGCCACC**ATGACGCTCCTCC**
CCGGCCTCCTGTTCTGACCTGGCTGCACACATGCCTGGCCACCATGACCCCTCCCTCAGG
GGGCACCCCCACAGTCACGGTACCCCACACTGCTACTCGGCTGAGGAACGTGCCCTCGGCCA
GGCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGCTTGCGCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCGGTGCTGCCGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAACGCTGGCCTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGACGGCCCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGTGCCTGCCGCCGCGCCCTGCTCCCGCGACGGCTGGGCT
CCCCACACCTGGGGCCTTGCCTTACACCGAGTTCATCCACGTCCCCGTCGGTGCACCT
GCGTGCTGCCCGTTCAGTGT**TGACCGCCGAGGCCGTGGGCCCTAGACTGGACACGTGTGC**
TCCCCAGAGGGCACCCCTATTATGTGTATTATTATTGTATTATGCCTCCCCAACACT
ACCCTTGGGTCTGGCATTCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGTAGAAGGAGCTCAGCACCTCTCCAGCCCTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGCTCCGGCTCCCTTACCTA
TCACTGGCCTCAGGCCCGCAGGCTGCCTCTCCAACCTCCTTGAAGTACCCCTGTTCT
TAAACAATTATTAAGTGTACGTATTAAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLFLTWLHTCLAHDPSLRGHPHSHGTPHCYSAEELPLGQAPPPLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVILEADTHQRSISPWRYRVDTDEDRYPQKL
AFAECLCRGCIDARTGRETAALNSVRLLQSLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCGACCTCACCAAGGAGAACATGCAGCTGGCACTGGCTCCTG
CTGGCCGCCGTCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCAACCAGTCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA
CTGCCACCCGGGTCTCAGCAACACCGAGGGATTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCGATATCCCCAGCCTGGCCTGGGCCCTACGTATCCATCGCTGCTGCCAGAC
CAGCCTCTGCAACCATGACTGACGGCTGCCCTCCAGGGCCCCGGACGCTCAGCCCCAC
AGCCCCCACAGCCTGGGCCAGGGCTCACGGCCGCCCTCCCTGAGACTGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGCCTAGGAAAGTCCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGCCCATCGCCTGCCGCCCTTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEEAIWCHQCTGGCShGSRCLRDSTHCVTTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD
```

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCACTTGTCAAGAGGCCGGGAAGAGAAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGCTTCGCTCGCCTCTAGGACATACACGGGACCCCT
AACTCAGTCCCCAACCGCGACCCCTCGAAGTCTGACTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGGCAGGTCCGGCGAAGGCGATGCGCGCAGGGGGTCGGCAG
CTGGGCTCGGGCGGGCGGGAGTAGGGCCCGCAGGGAGGCAGGGAGGCTGCATATTAGAGTC
GCGGGCTCGGCCCTGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGGAGCCCGTGGTCTCGTGCTGCTGGCGCCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTGCTGACTCAAGCATCCCTGCTA
CAAATGGCCTACTTCCATGAACGTCCAGCCGAGTGAGCTTCAGGAGGCACGCCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAACAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGACAGGGATTCTGATGGTGATTCTGGATAGG
GCTTGAGGAATGGAGATGGCAAAACATCTGGTGCCTGCCAGATCTTACCAAGTGGCTG
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTCCTGCGAACAGTAAAAAG
TGTGTTGTGATGTATACCAACCAACTGCCAATCCTGGCCTGGGGTCCCTACCTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTGCAAGTATGAACCAGAGATTA
ATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT
GTGGTTGTTACTGAAGCAGGTATAATTCCAATCTAATTATGTTGTTATACCAACAAATACC
CCTGCTCTTACTGATACTGGTTGTTGGAACCTGTTGTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAAAAACTAGTCCAAACCAGTCTACACTGTGGATTCAAAGAGTACCAAGAAAA
GAAAGTGGCATGGAAGTATAAACTCATTGACTTGGTCCAGAATTGTAATTCTGGATC
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTGAAATCACAAAGGATCTGCAA
GATGAACCTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTGTTATATGCTATTATTC
ATTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTGCTAAAGGATGCAC
CCAAACTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTGTATCACACACGTC
GGGAGTATGTGTGTTAGAAGCAATTCTTATTCTTACACCTTCATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTACAGTGTGCAAAAGTATTACCTTGCATAA
GTGTTGATAAAAATGAACGTGTTCTAATATTATTATTGTCATCTCATTTCATAACAT
GCTTTGATTAAAGAAACTTAACTGTGTTCTAATTTGTCATCTCATTTCATAACAT
TACCATAGAAAAAGTTGTTCTGAAATAATTGTCATCTCAGCTCTGCTTGTCA
ATGTCTAGGAAATCTCTCAGAAATAAGAAGCTATTGTCATTAAGTGTGATATAAACCTCCTC
AAACATTAACTTAGAGGCAAGGATTGTCATAATTCAATTGTCAAGACATGTGCCCTATAA
TTATTGCTAAACAGATTGTAATAATGTAACATTGTTAATAGGTGCATAA
ACACTAATGCAGTCATTGAAACAAAAGAAGTGACATACACAAATATAATCATATGTCCTCA
CACGTTGCCCTATATAATGAGAACAGCAGCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCACTAAACAAAGATGGTTGTTGGGTTGGATTGACACTGGAGGCAGATAGTGC
AAAGTTAGTCTAAGGTTCCCTAGCTGTATTAGCCTCTGACTATATTAGTATACAAAGAGG
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ATTAGGAAGGAAAGGAACACTGAAATCGTGTGAAATGGGTTGGAACCCATCAGTGTG
CATATTGATTGAGGGTTGCTTCAAGAGAAAGTTGTAACCTCTGGTCTTCA
TAGTTCTTCAATGCTTACGCCTGTTCTCAAGAGAAAGTTGTAACCTCTGGTCTTCA
TATGTCCTGTGCTCCTTTAACAAATAAAGAGTTCTGTTCTGGGGAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230
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><MW: 30431, pI: 6.79, NX(S/T): 3
MSRVVSLLLGAALLCGHGAFCRRVVSGQKVCFADFKHPCYKMAKFHELSSRVSFQEALACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSPNQSTLWISKSTRKESGMEV
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Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGA**ATGGAGAGAGCAGTGA**GAGTGGAGTCGGGGTCCTGGTCGGGTGGTCTGTCGTCCTGGCATGCCCTG
CCACAGCCACTGGGCCGAAGTGCTCAGCCTGAAGTAGACACCACCCCTGGTCGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTTCTGGGCATTCCATTGCCAGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACACCCAGCACAGCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTGCTCTAACCGAAAACAGCAGATCTCTCGGTTAGGCGGTATGGGTATGGGTCCATG
GCCTGGTCCTCAACGTCTAGCCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCGGTATGGTATGGGTCCATG
GAGGCCTCTGATAACTGGCGTGCACCTCACGATGGATCAGCTCTGGCTGCCTATGGGATGTGGCGTGG
TTACAGTCCAGTACCGCCTTGGGTCCTGGCTTCTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTGCCTGGTCAAGAAAACATGCCCTTCGGGGTAGCCTCAACTGTGTCA
CTGTCTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCTGGTCTCCAGTGGCTGCAGGGCTTCC
ACAGAGCCATCACACAGAGTGGGTATCACCAACCCAGGGATCATCGACTCTCACCCCTGGCCCTAGCTCAGA
AAATCGCAAACACCTGGCTGCAGCTCCCGCTGAGATGGTCAGTGCCTTCAGCAGAAAGAAGGAG
AAGAGCTGGCCTTAGCAAGAAGCTGAAAAAAACTATCTATCCTCACCCTGATGGCACTGTCTCCCCAAA
GCCCAAGGAACCTCTGAAGGAGAACGCCCTCCACTCTGTGCCCTCCATGGGTGCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGCTGGGTCTCTGGATACAATGGAGCAGATGAGCCGGAGGACATGCTGCCATCT
CAACACCGCTCTGACCAGTCTGGATGTGCCCTGAGATGATGCCACCGTCAAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAATGCCAGGGCTTCCAGGAATTCTGGTGCAGTATTCTCATCAATGTTCCACCGTCA
GTTTTCAAGATACCTTCAGGATTCTGGAGCCCTGTCTTTCTATGAGTTCCAGCATGCCAGTCTGGTCTTTG
CGAAGATCAAACCTGGCTGGGTGAAGGCTGATCATGGGCCAGGGTGTGTTGTTGGAGGTCCCTCCTCA
TGGACGAGAGCTCCCCCTGGCTTCCAGAGGCCACAGGAGGAGAACAGCAGTAAGCTCACCATGATGGGCC
AGTGGACCCACTTTGCCGGACAGGGGACCCCCAATAGCAAGGCTCTGCCCTTGGCCCAATTCAACCCAGGG
AACAAATATCTGGAGATCAACCCAGTGCCACGGCCGGACAGAAGTTCAAGGGAGGCTGGATGCAGTTCTGGTCA
AGACGCTCCCAGCAAGATAACAAGTGGCACCAAGCAGAAGAACAGGAAGGCCAGGAGGACCTC**TGAGGC**
AGGCCTGAACCTTCTGGCTGGGAAACCACTCTCAAGTGGTGGCAGAGTCCAGCACGGCACGCCCTCTC
CCCCCTGCTGAGACTTAACTCCACCAAGCCCTAAAGTGTGGCGCTCTGTGACTGGAGTTATGCTCTTTGAA
ATGTCACAAGGCCCTCCACCTCTGGGCATTGTACAAGTTCTCCCTCTCCCTGAAGTGCCTTCCCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCTCTAGCTTCTGGAGGACTCACTCCCCAGGAAGCCTCCCTGCCCTCTC
TGGGCTGTGCCGGCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTGCTGTCT
CCCCCTCAGAGGAGCTCTCAAAATGGGATTAGCCTAACCCACTCTGTCACCCACACCAGGATGGTGGGA
CCTGGAGCTAGGGGTGTTGCTGAGTGAGTGAGTGAACACAGAATATGGAATGGCAGCTGCTGAACCTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCAACCGACATTGTCCACCCCTGGCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGATGGAGAAGTCTGGGCGCCAGGGATCCAGCCTAGAGCAGACCTAGCCCCTGAC
TAAGGCCTCAGACTAGGGCGGGAGGGTCTCTCTCTGTGCTGCCAGTCTGGCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTCAACCCAGACCTGACCCCTACCAATTCCAGGCCCTGACCCCTCAGGACGCTGGATG
CCAGCTCCAGGCCAGTGCCTCCCTCCCTCTGGCTGGGAGACCAAGTTCTGGGAGCTTCAAG
AGCACCCACCAAGACACGAGGACAGGCCAGGGAGGGCATCTGGACCAAGGGCTCCGTCGGCTATTGTACA
GAGAAAAGAAGAGACCCACTGGGCTGCAAAAGGTGAAAGCACAAGAGGTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGGCCCTCACAGCCCTCGCTGCTCTCCCTGCCCTCTGGCTGGCCACTTGGCA
GCACTTGAGGAGGCCCTCAACCCGCCGCTGCACTGTAGGAGCCCTTCTGGCTGGCCAAGGCCGGAGCCAGCT
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AGTGAGTTCCGGGTGGCGTGGCTCGGCCGGCCCCACTCAGAGCAGCTGCCGCCAGGAGTGGCAGTGGCCT
TAGCACCTGGGCCAGCTGCTGTGCTGATTTCTGCTGGGCTTAGCTGCTCCCTGCCGGGGCAGGGCTCG
GACCTGCAAGCCCTCCATGCCGTACCCCTCCCCCACCCCCCTGGCTCTGTGCGGCCGGAGCCTCCCCAAGGAG
CGCCGCCCTGCTCCACAGGCCAGTCCATGACCACCAAGGGCTGAGGAGTGCCTGGTGCACAGGCCGGGA
CTGGCAGGCAGCTCACCTGCTGCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGCTCTGAGTCTGGTGG
GGACTTGGAGAACCTTATGTCTAGCTAAGGGATTGTAATACACCGATGGCAGCTGTATCTAGCTCAAGGTT
TGTAAACACACCAATCAGCACCTGTGCTAGCTAGTGTGATGCACCAATCCACACTCTGTATCTGGCT
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TTGTGTCTAGCTCAGGGATGTAAACGCACCAATCAGCACCTGTCAAAACAGACCAACTTGACTCTGTAAAAT
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTGGGTCCCCCTCCACGCCGTGGAAGCTTGTGCTCTTGCAATAATCTTGCTACTGCCAAAAA

FIGURE 12

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><subunit 1 of 1, 571 aa, 1 stop
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IPFA QPPLGPDRFSAPHAPQWPWEGVRDASTAPPMLQDVEMNSRFVLNGKQQIFSVD
LVNVYSPAEPAGSGRPVMVVHGGALITGAATSYDGSALAAYGDVVVTVQYRLGVLGFF
STGDEHAPGNQGFLDVVAALRWVQENIAFPFGDLNCVTVFGGSAGGSIISGLVLSPVAA
HRAITQSGVITTPGIIDSHPWPLAQKIANTLACSSSPAEMVQCLQQKEGEELVLSKKLN
TYPLTV DGTVPKSPKELLKEKPFHSVPFLMGVNHEFSWLI PRGWGLLDTMEQMSREDMLA
ISTPVLTSLDVPPEMMPTVIDEYLGSNSDAQAKCQAFQE FMGDVFINVPTVSFSRYLRDGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQKQKNRKAQEDL
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTGCAGCTTACCGCTAAAATGTTCCGGGCCAGAGCAAAGGTATTGCAG
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTCTACAACATAAAATTCTCAAA
CCTAAAATCAACAGCTTTATGCCTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTCTCT
GGAAAAGTATAAAGGCAAAGTTCACTAGTTGTAAACGTGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAAC TGACAAAGAGTTGGACCATCCCAC TT CAGCGTG
TTGGCTTTCCCTGCAATCAGTTGGAGAACCTGGAGCCAGCAAGGAAGTAGAATC
TTTGCAAGAAAAACTACGGAGTAACCTCCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTAGATTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTGGAAGTATCTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGTACATAAAAAGAAAG
AGGATCTATGAATGCCATTGCGTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTG
GTCTCATTAAACATTTTTGGAGACAGTGTCTCACTCTGTCAACCAGGCTGGAGTG
CAGTAGTGCCTCTCAGCTCATTGCAACCTCTGCCTTTAAACATGCTATTAAATGTGGCA
ATGAAGGATTTTTAATGTTATCTGCTATTAAAGTGGTAATGAATGTTCCAGGATGAG
GATGTTACCCAAAGCAAAATCAAGAGTAGCCAAGAACATGAAATATATTAACTACT
TCCTCTGACCATACTAAAGAATT CAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTCTAGGACTGTACTGATGAAAATGCCAACACACTAGACCACTCTT
GGATTCAAGAGCACTGTGTATGACTGAAATTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTGTTGTACAGGATTTGTTTTAAGTACAGGTTCTAGTGTGTTT
ACTATAACTGTCACTATGTATGTAAC TGACATATAAATAGTCATTATAAATGACCGTAT
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAA

FIGURE 14

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL
EKYKGKVSLVVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFCPCNQFGESEPRPSKEVES
FARKNYGVTFPPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP
IEVIRPDIAALVRQVIKKKEDL
```

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

FIGURE 16

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145
><subunit 1 of 1, 888 aa, 1 stop
><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLGGAHGLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA
DDLNIQRVLRVNRTLFIGDRDNLYRVELEPPSTELRYQRKLTWRSNPSDINVCRMKGKQEG
ECRNFVKVLLLRDESTLFVCGSNAFPVCANYSIDLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWSHVYFFFREI
AMEFNYLEKVVVSRRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVGDHFYFNVLQAVTG
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAASFEGRFREQKSPEIWT PVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTGLSVFLEEFTYRPDRCGRPGGGGETGQ
RLLSLELDAASGGLLAAFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG
TRAafeQDVSGASTSGLDCTGLRASLSEDRAGLVSVNLLVTSSVAAFFVVGAVVSGFSVGV
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDGLLPTPEQTPLPQKRLPTPHPHHALGPRAWDHGHPLLPA
SASSSLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRVVSAPTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRHTFNSGEARPGDRHRGCHARPG
TDLAHLLPYGGADRTAPPVP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTCATCATTGTCCTGAGAGAGAGGGAGCAGCGCGGTTCTGGCCGGGACAGC
AGAACGCCAGGGGACCCTCACCTGGCGCGCCGGGCACGGGTTGATTGTCCTGGGTGCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGCGCAACCTTGAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTCTGTCCACCTCTACACTCTTC
ATTTATCGGTGGATCATTGAGAGTCGCTTGTAATGTTGGCACTTGCTACTTTATT
GCTTCTTCTGGCGACAGTCCAGCAGTCGCCAGACCGGGAGAAAGGCAGCTGAGCCCG
GAGAAGAGCGAAATATGGGGACCCGGCTAAAAGCAGACGTCGTCCTCCGCCGCTATTT
CTATATTCAAGGCAGTGGATAACATCAGGGAAATAATTACATCTCTCCAGGCAGGGTCT
TCCAGGTGAAAGTCTCAGCACCAAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTAGAC
CGAAAAGATGGGCCTTCATAGTAAGATAACAGAATGTATGCAAGCTACAAAATCTGAAGGT
GGAAATTAAATTCCAAGGGCAACATGTGGCAAATCCCCATATATTTAAAAGGGCCGGTT
ACCATGAGAACTGTGACTGTCCTCTGCAAGATAAGTCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAAGAGAGATCTGGCACATTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCAAAAGATTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA
AGGATAACAAGGTTATATCAAGACTCATGGTGAACATGTAGGTTAGAATTTCATGGAT
GCCATACTACTTCTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTTTGTTAATT
GGGAGACTGGCCTTGGAAAAAAAGAAATCCAATTCAAACATCCATCGATCTTCCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTGTGACTGCCTACGTACGATTGACTGATTCTGTTCTG
GAAACCATGGCCGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGCTCCCTG
GGAAAGCAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGAAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTCACCAACTTTCTTC
TTAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTCATTTTGATTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTATCGCCTGCCATATTG
TAGTTGGTACAGTGTTGCTGAAGCAGGATTCCATCTACTATGAACATTTCACAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT
TAAATGGCGAAAGATCACGATGAAGAGGCCAAAAGATAGCAAAAGCAGGACAAGAATTG
CAAGAAATAATCTCATGGCGATGACATATTCTGTTATTATTCAAACTTTCCAGGAATAT
GCCAATTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAGGGTAGAACACAGAC
TGAGGACGACCTCTCCCTGTACTGCCATAGGAAAAAGACCAAAAGATGAACTCTGAT
CAAAATAACTCTATTAGAATAATGGTGTGCTGAAGACTCTTCTTAACAAAAAGAAGAATT
TTTTAAGTATTAATTCCATGGACAATATAAAACTGTGTGATTGTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTAAAGTACATTGTTAGAATTAA
TAAAACCACCTTATTTAAAGGAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917
><subunit 1 of 1, 502 aa, 1 stop
><MW: 58043, pI: 7.94, NX(S/T): 2
MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVL PARYFYIQAVDTSGNKF
TSSPGEKVFQVKVSAPEEQFTRGVQVLDRKDGSIIVRYRMYASYKNLKVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDSAALREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDWPLEKKKSNS
NIHPIFSWCGSTDSDKDIVMPTYDLTDVLETMGRVSLSMMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPELIDAFTNFFFKHDENLYGPIVKHISFFDFFKHYQINIDGTV
AAYRLPYLLVGDSVVLQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLWAKDHDEEAKK
IAKAGQEFAARNNLMGDDIFCYYFKLFQEYANLQVSEPOIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL
```

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCGGTCCGCATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGCTCCGGACTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTCCTCGGGATTCTCCCGCTCCGTTGCTCTGCC
AGAGCGGAACACGGAGCAGCCCCAGCGCCGAACCCTCGGCTGGAGCCAGTTCTAAGT
GACCACGCTGCCACCACCTCTTCAGTAAAGTTGTTATGCTGATAGATGCCTTGAGAG
ATGATTTGTGTTGGGTCAAAGGGTGTGAAATTATGCCCTACACAACCTACCTTGAGAA
AAAGGAGCATCTCACAGTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTCCTGGCTTGTGACGTATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTT
TATGGAGATGAAACCTGGGTTAAATTATTCCAAAGCATTGTGGAATATGATGGAACAAC
CTCATTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTGGATAAAG
TATTAAAAAGAGGGAGATTGGGACATATTAATCCTCACTACCTGGGCTGGACCACATTGGC
CACATTCAGGGCCAACAGCCCCCTGATGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCACTGAGGAGAGAGAGACGCCTTACCAATTGCTGG
TTCTTGTTGACATGGCATGTCGAAACAGGAAGTCACGGGCTCCTCACCGAGGAG
GTGAATACACCTCTGATTTAATCAGTTCTGCTGTTGAAAGGAAACCCGGTATATCCGACA
TCCAAAGCACGTCAA**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTACATTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAGATCCTGGGTTGAGCAGTTAAAATGTCAGAAAGATTGCATGGGAAC
GGATCAGACTGTACTGGAGGAAAAGCATTGAGCAGCTTACACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGACAAAGTGGCCA
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT
CCCACTGTCATCCTGGTTCTGCTCTTTATTGGTGTACCTGGTCTTCTGGCC
TTCACGTCATTGTTGACCTCAGCTGAAAGTTGCTACTTCTGTTGACACCTGGTGTGCCAAGTGGCTG
GGGGCAGGCTGCCTTCGTTACAGACTCTGGTGAACACCTGGTGTGCCAAGTGGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAAGGACGTTGAGCAGCCTTATCCCAGGCCTCTGGG
TGTCCCACACAGGTGTTACATCTGCTGTCAGGTGAGATGCCTCAGTTGAAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAGAGCTGGCGGTACAGAGGAACAAAGGCC
CCCAGCTGAGGGGGTGTGAATCGGACAGCCTCCCAGCAGAGGTGAGGCTGAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTGGTCGCACCA
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTCTTCAAGGCGGA
CGTTTCTGTTGAAATTCTTAGTCCTGGCCTGGACACCTTCATTGTTAGCTGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGGGGATGGTCACACTCAGATCCACAGAGGCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCCCTGCACAGCCCTCATC
CCCTCTGGCTTGAGCCGTCAAGAGGCCCTGTGCTGAGTGTGACCGAGACACTCACAGCTT
TGTGATCAGGGCACAGGCTCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGC
CCATCTGGCTCATGCTCTCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

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><subunit 1 of 1, 310 aa, 1 stop
><MW: 33875, pI: 7.08, NX(S/T): 2
MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTLLPP
PLFSKVIVILIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWKLFPKHFVEYDGTSFFVS
DYTEVDNNVTRHLDKVLKRGDWLILHHLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ
```

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAAT
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTGAGGCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCACAGCTTGAGCACACCTACTTGGCCCTTGACCTCAGGGCCATG
AAGCTGCCAGCATCTCCTGTCCATGAGTGCTTGAGGCTATCCTGTCTGGACACCGG
GTATCGCGGCCGGTGACCTGGTGCAGGAAGGGCTGCTGGACCAGGGCTCCTGCAGGGCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCAGGGCTGCACAACGTAC
AAATGCAACGCCACCTCATGACTCATGACGCCCTCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCCGAGTGCTACGCCCTGTATCGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCCGACGAGTCCAGTGTACCCAGGACCAGACGCCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCAACGAGGGCACCACCAAGCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTCACCAAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCCTGGCCCTGCTCCCTCCAGTCCTCCTGCTGGTGGGCTCTCAGC
ATAGACCGCCCTCCAGGATGCTGGGACAGGGCTCACACACCTATTCTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

```
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><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
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DTGYRAPVTLVRKGCTGPPAGQTQSNSPDALPPDYSVVRGCTTDKNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATPPRALQVLALLPVLLLVGLSA
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCACCGTCCGGGACAGATGAACCTAAAAGAGAAGCTTAGCTGCCAAAGATTGGAAAGG
GAAAGGACAAAAAAGACCCCTGGCTACACGGCGTAGGTGCAGGGTTCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCT**ATGGCTGT**
CAGAGAGTTGTGCTTCCAAGACAAAGGCAAGTCCTGTTCTTTCTTTGGGAGTGT
CCTTGGCAGGTTCTGGTTGGACGTTATCGGTGACTGAGGAAACAGAGAGAAAGGATCCTT
GTGGTCAATCTGCCAAAGGATCTGGACTAGCAGAGGGGAGCTGGCTGCAAGGGAACAG
GGTGGTTCCGATGATAACAAACAATACCTGCTCTGGATCACATACCGGAATTGCTCA
CAAATGAGAAACTGGACCGAGAGAAGCTGTGTCGGCCCTAAAGAGCCCTGTATGCTGTATTC
CAAATTTAATGGATGATCCCTTCAGATTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACCGGCCAGTATTTCAGGACAAAGAAACAGTCTAAAAATATCAGAAAATACAGCTG
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AACTACACGATCAGCCCCAACTCTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGAGGAGCAGGGAGAGCTCAGCT
TAACCCTCACAGCGCTGGATGGTGGTCTCCATCCAGGTCTGGACCTCTACTGTACGCATC
GTTGTCTTGGACGTCAATGACAATGCCAACAGTTGCCAGGCTCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGTTCTTATTGTTAAGGTATGGCAGAAGATGTAGACTCTG
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CAAATCAATCCTTTCTGGGAAATCTTCTCAGAGAATTGCTGATTATGAGTTAGTAAA
TTCTTACAAAATAATATACAGGCAATGGACGGTGGAGGCCTTCTGCAAGATGTAGGGTT
TAGTGGAAAGTATTGGACACCAATGACAATCCCCCTGAACGTGATCATCATTTCCAAC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGTGTGTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAGATGGTTGCTACATTCAAGAGAATCTGCCATTCTACTAAACCTT
CTGTTGAGAATTTCACATCTAATTACAGAAGGCCGCTGGACAGAGAGTCAGAGCCGAG
TACAACATCACTATCACCGTCACTGACTTGGGACACCAGGCTGAAAACCGAGCACACAT
AACGGTCTGGTCTCCGACGTCAATGACAACGCCCGCCTCACCCAAACCTCTACACCC
TGTCGTCGCGAGAACAAACAGCCCCGCCCTGCACATCGGCAGCGTCAGGCCACAGACAGA
GACTCGGGCACCAACGCCAGGTACCTACTCGCTGCTGCCGCCAGACCCGCACCTGCC
CCTGCCCTCCCTGGTCTCCATCAACCGGACAACGCCACCTGTTGCCCTCAGGTCGCTGG
ACTACGAGGCCCTGCAGGTTGAGTTCCGCGTGGCGCCACAGACCGCGCTCCCCCGCG
CTGAGCAGAGAGGCCGCTGGTGCCTGGTGTGGACGCCACGACAACCTGCCCTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCCCTGCACCGAGCTGGTGCCCGGGCGGCGAGC
CGGGCTACCTGGTACCAAGGTGGTGGCGGTGGACGGGAGCTGGGCCAGAACGCCCTGGCTG
TCGTACCAAGCTGCTCAAGGCCACGGAGGCCGGCTGTTGGTGTGGCGCACAATGGGA
GGTGCACCGCCAGGCTGCTGAGCGAGCGCAGCAGCAAGCACAGGCTGTTGGCTTG
TCAAGGACAATGGCAGGCCCTCGCTCGGCCACGCCACGCTGCACTGCTCTGGTGGAC
GGCTTCTCCCAGCCCTACCTGCCCTCCGGAGGGGGCCAGGCCAGGCCAGGCCAGGC
CGACTTGCTCACCGTCTACCTGGTGGTGGCCTCGGTGTCTCGCTCTCCCTCT
CGGTGCTCCTGTTGCGGGCTGTCAGGAGGAGCAGGGGGCCCTCGGTGGTGGCTG
TGCTCGGTGCCGGAGGGCTTCCAGGGCATCTGGTGGACGTGAGGGGGCGCTGAGACCC
GTCCCAGAGCTACCAAGTATGAGGTGTCTGACGGGAGGCCGGACCAGTGAGTTCAAGT
TCTTGAAACCACTATTTCGGATATTCAAGGCACAGGCCCTGGAGGAAGGGTGAAGAAAAT
TCCACCTCCGAAATAGCTTGGATTAAATATTCAAG**TAAAGTCTGTTT**TAGTTCATATAC
TTTGGTGTGTTACATAGCCATGTTCTATTAGTTACTTTAAATCTCAAATTAAAGTTAT
TATGCAACTTCAAGCATTATTTCAAGTAGTATAACCCCTGTGGTTACAATGTTCATCAT
TTTTGCATTAATAACAACGGTTAATTAAATGAGTATTCTAAATGATAGTGT
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CTGAGGTTTGATTCAATTCAAGAGCTGCGATCTCATGATTCTAATCACTTCTGTCTATAGT
TACTTGCTCTATTAAGAAGGCATATCTACATTCCAAACTCATTCTAACATTCTATATATT
CGTGGTAAACCATGTCATTATTCTACATCATGTATTAAAAAGAAATATTCTCTAC
TACTATGCTCATGACAAATGAAACAAAGCATATTGTGAGCAACTGAAACATCAATAATAC
CCTTAGTTATATACTTATTATTTATCTTAAAGCATGCTACTTTACTTGGCCAATATTT
CTTATGTTAACTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA
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FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

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DINDHAPVFQDKETVLKISENTAEGTAFRLEERAQDPDGGLNGIQNYTISPNNSFFHINISGGD
EGMIYPELVLVDKALDREEQGELSLLTALDGGSRSRGTSTVRIIVVLDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVWAEDVDGVNAEVSYSSFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAMDGGGLSARCRVLFVLDTNPPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGKVMVCYIQENLPFLKKPSVENFYILITEGALDREIRAEYNITITVTDLGPRLKTE
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDGTNAQVTYSLLPPQDP
HLPLASLVSINADNGHFLALRSLDYEALQAFEFRVGATDRGSPALSREALVRVLVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAO
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSPPEGFPGLVLDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 25

GAATGAATACTCCGAAGCCGTTCTCCAGATGTGAATAGCTCCACTATACCAAGCCTC
GTCTTCCTTCCGGGGACAACGTGGTCAGGGCACAGAGAGATATTAAATGTCACCCCTTG
GGGCTTCATGGACTCCCTCTGCCACATTGGAGGTGGAAAGTTGCTAGAGGCTTC
AGAACTCCAGCCTA**ATGG**ATCCCAAACCTGGGAGAATGGCTCGTCCCTGCTGGCTGTGCTG
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGGCGCTGTTAGAGAA
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTGTGCAAGACGCTGAAGGAGTGGTGG
CCATCGAGAGCGACTCTGTCAGCCTGTGCAGCGCTGGGGGCCGTGCGCTGGACATGGTCC
GCCGTGGCTGCAGACACGCTGCAGCGCTGGGGGCCGTGCGCTGGACATGGTCC
TCAGCAGCTGCCGATGGTCAGAGTCTTCCAATACCTCCGTATCCTGGCCGAACGGG
GCGATCCCACGAAAGGACCGTGTGCTTACGGCACTTGGACGTGCAGCCTGCTGACCGG
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGAAACTTATGGACG
AGGAGCGACCGACAACAAAGGCCGTCTGGCTGGATCAATGCTGTGAGCGCCTCAGAG
CCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATGAGGGGATGGAAGAGGCTGGC
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CATTGTAATTCAGATAACCTGTGGATCAGCAAAGGAAGCCAGCAATCACTATGGAACCC
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTCACTCAGGAACC
TTTGGTGGCATCTTCATGAACCAATGGCTGATCTGGTGTCTTCTCGGTAGCCTGGTAGA
CTCGTCTGGTCATATCCTGGCCCTGGAATCTATGATGAAGTGGTCCTCTACAGAACAGG
AAATAAAACATACAAAGCCATCCATCTAGACCTAGAAGAACCGGAATAGCAGCCGGGTT
GAGAAATTCTGTTGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT
TTCTATTCTGGAATCGAGGGCGCGTTGATGAGCCTGGAACCTAAACAGTCATACCTGGCC
GAGTTATAGGAAAATTTCATCCGTCTAGCCTCACATGAATGTTCTGGGAA
CAGGTGACACGACATCTGAAGATGTTCTCCAAAAGAAATAGTCCAACAAAGATGGTGT
TTCCATGACTCTAGGACTACACCGTGGATTGCAAATATTGATGACACCCAGTATCTCGCAG
CAAAAGAGCGATCAGAACAGTGGTGGAAACAGAACCGAGATATGATCCGGATGGATCCACC
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTCTAATTCCGCTGGG
AGCTGTTGATGATGGAGAACATTGCGAGAACATGAGAAAATCAACAGGTGGAACTACATAGAGG
GAACCAAATTATTGCTGCCTTTCTTAGAGATGGCCAGCTCCATTAAATCACAAGAACCT
TCTAGTCTGATCTGATCCACTGACAGATTCACCTCCCCACATCCCTAGACAGGGATGGAAT
GTAAATATCCAGAGAATTGGGTCTAGTATAGTACATTTCCTCCATTAAAATGTCTTG
GGATATCTGGATCAGTAATAAAATATTCAAAGGCACAGATGTTGAAATGGTTAAGGTCC
CCCACTGCACACCTCCTCAAGTCATAGCTGCTGCAGCAACTTGATTCCCCAAGTCCTGT
GCAATAGCCCCAGGGATTGGATTCTCCAAACCTTTAGCATATCTCAACCTGCAATTGA
TTGGCATAATCACTCCGGTTGCTTCTAGGTCTCAAGTGCTCGTACACATAATTCC
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AAAAAA

FIGURE 26

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GTVCFYGHLDVQPADRGDGWLTDYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAYEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH
```

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTAAAGGTTGCCGCTAGCCGCCTGGGAATTAAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTAGACGGCGCTTGTCATGGGACCTGTGCGGTT
GGGAATATTGCTTTCTTTGGCCGTGCACGAGGCTGGCTGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAAC TGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTACAGCCTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTATGTGAGCGGATCCTGGACTATAGTGTTCACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG
GGTGAAGGTGGATCTGGGATCCCTCTGGAGCTTGGATGAGCCCAGCGTGGAGGTACAT
ACCTCAAGAACAGCAGTGTGAGACCATGTTGGAGGAGTTGAAGACATTGTGGAGACTGGTAC
TTCCACCACATCAGGAGCAGCCCCTACAAAATTTCTGTGAAGGTACATGTGCTCCCAGCTGC
TGAAACTGCATGTCTACAGGAAACTTGGACTGGAAAGGAGATCACAGATGGGAAGAGAAAA
CAGAAGGGAGGAAGAGCAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCAAACTTGACCGAGAACATCTTTGACCCTGCCTTGAG
CCCCCAGGAGGGAAAGGGATCATGGAGAGCCCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTCAGGGTGTGTTATGAGTGA CACTCCACCAAGCTTGTAGCTGTTCTCTCCATCTAAC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTCTGGGTGGAGGGTGGGGTGGAGG
TCCTGCTCCTAGAGATGA ACTCTATCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTCCCTTTAACTGATCCCACCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGCTTGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTAGACCCTCAAGGAAGA
GGCCAGAACGGACATTCTCTGCATCTATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGTCATGGCCTGGAGTTGCTGATAATTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTATAGGT
GCTCAACTTCTATATCGCTATTAAACTTTTTCTTTCTA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAEELSRTGRSREVL
ELGVQLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSLRYAKGQSQTMATLK
GLVQKGVKVDLGIPLWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQQPLQNFLCEG
HVLPAETACLQETWTGKEITDGEKTEGEEEQEEEEEEEGGDKMTKTGSHPKLDREDL
```

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCGGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCACAGAGTCCCC**AT**GGGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCC GTG GCCATGA
GGCCCTCTGGACGAGGACACCCTTTGCCAGGGCCTTGAAGTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAAC TACAGACAGAACAGATCAC CCTGG
ATGGAGCCGATAGTCAAGTTCCGGGGCCGTGGACGGCGAACCTATATCCTGGTATGGT
GGATCCAGATGCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGAAGATT CAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTGTCTATCTCA
GGAAGGAAAAGTCATCTCTCCCTCCAAGGAAAACAAACTCGAGGCTCTGGAAAATGG
ACAGATTCTGAACCGCTTCCACCTGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCCTCCAGGCTCCAGAGGAAGGGCCAGCGAGCCAAAGCACAA
AACCCAGGCAGAGA**TAG**CTGCCTGCTAGATAGCCGGTTGCCATCCGGCATGTGGCCACAC
TGCTCACCAACCGACGATGTGGGTATGGAACCCCTCTGGATA CAGAACCCCTTCTTTCAA
ATTAAAAAAAATCATAAA

10
9
8
7
6
5
4
3
2
1

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274
><subunit 1 of 1, 223 aa, 1 stop
><MW: 25402, pI: 8.14, NX(S/T): 1
MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDETLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRWLVTDIKGADLK
KGKIQQQELSAQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCACTCCCCTGGACTGTAGATAAAGA
CCCTTTCTGCCAGGTGCTGAGACAACCACACTATGAGAGGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTATTTGGGAATCCAGAAATCCAGAAATGTGTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAACCCCTCCTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCCTGAGTCTGTGGCCTCCCGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAAACACTGCCTTGAAATTAAATATAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTGGTCTTGTCTAAAGTTCTGGTCCCAATGTGT
TTTCGTCTACATTTCTTAGTGTCACTTCACGCTGGTGCTGAGACAGGGAGCAAGGCTGCTG
TTATCATCTCATTTATAATGAAGAAGAAGCAATTACTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAACAGGAGAGCTGGGTGGTATAAGGCTGTCCTCAAGCTGGTGCTGTG
GCCACAAGGCATCTGCATGAGTGACTIONTAAGACTCAAAGACCAACACTGAGCTTCTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTGTTCTGTTGCTTATTCCCTCTGGGATGATATCATCCAGTCTTAT
ATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTAGCATTAAAGACCTTGAAACA
AAAATAATTCTGGGTGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTCTGTTGCTTATTCCCTCTGGGATGATATCA
TCCAGTCTTATATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTAGCATTAAAG
ACCTTGAAACAAAATAATTCTGTGTTAAGTTAAATCATTGCTTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTGTGTTATTTATATAATAATAAGCTAAAACGTATATAAA
ATAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFLFYRAKTGRSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACCATGAGGACGCCTGGCCTCTGCCCGTGCTGCTGCTG
CTCCTGGCGGGAGCCCCCGCCGCGGCCACTCCCCGACCTGCTACTCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACTGCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTGCCCGTGTGGAAAGTGGCCAGGTAGATTCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTGGTATTCTGTTGG
ATGACTGCAATGCCCTTGAATACCAATCCCAGTGACTACGGTCTGCCAGATCGTCAGCGC
TAAGGGAAC TGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCTACCCAGGAACCTCCTTGAGCATAGA
GTTAGCAACCATGCTCTCATTCCCTGACTCATGTCTGCCAGGATGGTAGATAACACAGC
ATGTTGATTGGTCACTAAAAAGAAGAAAAGGACTAACAAAGCTTCACTTTATGAACAACTA
TTTGAGAACATGCACAATAGTATGTTTATTACTGGTTAATGGAGTAATGGTACTTTA
TTCTTCTTGATAGAACCTGCTTACATTAAACCAAGCTCTATTATGCCTTTCTAACAC
AGACTTTCTCACTGTCTTCATTAAAAAGAAATTAATGCTCTTAAGATATATATTTACG
TAGTGCTGACAGGACCCACTCTTCATTGAAAGGTGATGAAAATCAAATAAGAATCTCTTC
ACATGGA

1002604
1420604

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011
><subunit 1 of 1, 136 aa, 1 stop
><MW: 15577, pI: 8.88, NX(S/T): 0
MRTPGPLPVLLLLAGAPAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDARKLYTIMNSFCRRDLVFLLDDCNALEYP
IPVTTVLPDRQR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCCTACCTGGAGA
CTTGACTCCGCGGCCAACCTGTTATCCCTGACCGTCGAGTGTCAAGAGATCCTGCA
GCCGCCAGTCCCGCCCCCTCTCCGCCAACACCACCCCTCCTGGCTTCTGTTTAC
TCCTCCTTTCATTCATAACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCA
AGCCGAGCGTGGAAAGAATGGGGTCTCGGGACCGGCACTTGGATTCTGGTGTAGTGC
CGATTCAAGCTTCCCCAACCTGGAGGAAGCCAAGACAAATCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTGAATGAACAGATTGCTGAAGCAGAAGACAAGAGATAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTAGAGCAACTATTCTTGTGATAACTGAACCTGC
TAAAGGAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAGATGTTGATTCAACCAAGAATCGAAAAGTGCATGA
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGCTGCCAGGATTAT
GAAGAAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCAAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAATACCAAGAGAAAAGTGAATGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTGGAAAGGAGAACTA
AAACCTACAGTGAAGACAACCTTGAGGAACCTCAATATTCCAAATTCTATGCGCTACTG
AAAAGTATTGATTGAGAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC
ACTGATTGACTTGTGAAGATGATGGTAAATATGGAACAATATCTCCAGAAGAAGGTGTT
CCTACCTGAAAACCTGGATGAAATGATTGCTCTCAGACCAAAACAAGCTAGAAAAAAT
GCTACTGACAATATAAGCAAGCTTCCCAGCACCACAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGAGCTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTAT
TTGGAAGCCATCAGAAAAAATTGAATGGTGAAGAAACATGACAAAAGGGAAATAAAGA
AGATTATGACCTTCAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGA
AAGGCATCCTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAA
TGGCAAAAGATCCAGGAGTCTTCAACTGTTCAGAAAACATAATATAGCTAAAACACTTC
TAATTCTGTGATTAATTTGACCCAAGGGTTATTAGAAAGTGTGAATTACAGTAGT
TAACCTTTACAAGTGGTAAAACATAGCTTCTCCCGAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPITAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPFKVTPMAAIQDGLAKGENDET
VSNTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNLEKNATDNISKLFPAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKNDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 37

GTTGCTCCGGCGGCCTCGGGGAGGGAGCCAGCAGCCTAGGGCTAGGCCGGGCCACC**ATG**
GCGCTGCCTCCAGGCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTGAG
CTCAGGGTGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGCTGAGCAGGGCACTTC
GGGAGAATGAACGCCACGCCCTCACCTGCCGGTGGCAGGGGGCTGGCACCCCCAGATTG
GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG
GGAGGCCCTCTGGAGGCCACCAGCACCTCACTGTCAGTCCCCTGCCATCGGGCCAGCATGAGC
TCAACTGCTCTGCAGGACCCCAGAAGTGGCGATCAGCCAACGCCCTGTGATCCTTAAT
GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGGCCAAGTACCAAGGAAGCTCAGGGCCAGG
CCTCCTGGTTGTCCTGTTGCCCTGGTGCCTGCCAACCGCCGGCCAATGTCACCTGGATCG
ACCAGGATGGGCCAGTGAATGCAACACCTCTGACTTCTGGTGCTGGATGCGCAGAACTAC
CCCTGGCTCACCAACCACACGGTGCAGCTGCAGCTCCGAGCCTGGCACACAACCTCTCGGT
GGTGGCCACCAATGACGTGGGTGTCACCAGTGCCTCGCTCCAGCCCCAGGGCCCTCCGGC
ACCCATCTCTGATATCAAGTGAATCCAACAACTAAAACCTCAACAAACGTGCCCTGCCACGG
GAGAACATGTCCCTCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATCCAGAGCAGT
GAAACCAGCAGACCGGCAGATGGCTCAGAACAAACAGCCGGCAGAGCTCTGGACCCGGAGC
CCGGCGGCCTCCTCACCAAGGTTCATCCGCTCCAGTGCCTGGCTATATCTATCGA
GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTC**TGA**GCCGAGGGCAGACAGGAGTATTCTC
TTGGCCTCTGGACACCCCTCCATTCTCCAAGGCATCCTCTACCTAGCTAGGTACCAACGT
GAAGAAGTTATGCCACTGCCACTTTGCTGCTGCCCTGGTGGGGTGCCTCCATGTCATG
CACGTGATGCATTCACTGGCTGTAACCCGAGGGCACAGGTATCTTGCAAGGCTACC
AGTTGGACGTAAGCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGCCCTT
CCAGAGGGAGCTCTTGCCAGGGGTGTTCAAGATGTCATCCAGCATCCAAGTGTGGCATGGC
CTGCTGTATAACCCACCCAGTACTCCACAGCACCTGTACAGTAGGCATGGGGCGTGCCT
GTGTGGGGGACAGGGAGGGCCCTGCATGGATTTCTCCTCTATGCTATGTAGCCTTGT
CCCTCAGGTAAAATTAGGACCCCTGCTAGCTGTGAGAACCCAATTGCCCTTGACAGAAA
CCAACCCCTGACCCAGCGGTACCGGCCAACACAAACGTCTTTGCTGACACGTCTCTG
CCCTCACTCTCTCTGTCCCCACCTCCTGGAAATTCTAGGTTACACGTTGGACC
TTCTCTACTACTCACTGGGCACTAGACTTTCTATTGGCCTGTGCCATGCCAGTATTAG
CACAAAGTTAGGGAGGAAGAGGCAGGCATGAGTCAGTAGCACCCAGGACGGCTGTAGCTA
TGCATCATTTCCTACGGCGTTAGCACTTAAGCACATCCCTAGGGAGGGGTGAGTGAG
GGGCCAGAGCCCTTTGGCTCCACGTTGGCCTCTGGGATTCACTGTGAGTGTC
CTGAGCTCTGGGGTTGATGGTTTTCTCAGCATGTCTCCTCCACCACGGGACCCAGCC
CTGACCAACCCATGGTGCCTCATCAGCAGGAAGGTGCCCTCTGGAGGATGGTCGCCACA
GGCACATAATTCAACAGTGTGGAAGCTTAGGGGAACATGGAGAAAGAAGGAGACCACATAC
CCCAAAGTGACCTAACACTTAAAGAACATGTAATGATTGGAAATTAAATATAGTA
CAGAATATATTTCCTGTTGAGATCTCTTGTAAATGTTTCACTGTACTGCCTAGG
GCGGTGCTGAGCACACAGCAAGTTAATAAAACTGACTGAATTCACTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGGTPR
LAWYLDGQLQEASTSRLLSVGGAEFGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVLFALVRANPPANVTWIDQDGPTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSAASLPAPGPSRHPSLISSDSNNKLNNVRLP
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCTGGGCCGAGGGGCTGGAGCCGGCCGGCGATGTGGAGC
GGGCCGCGGGCTGCCTGGCCGGTGTGTTGGGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCAAGACCAGGTCGGAGCTCGTACCTGCGGGTCGGTGTGAAGCTGCTC
AATACGCACCACCGCGTGCAGCTGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCTAGAGGCGTGGACGACGCCAATAGCTACTGGCGGATCCGGCG
GCTCGGAGGGCGGTGCCGCGGGTCCCCGGTGCCTGCGCTGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGCAAGAACCTGCACACGCACCACTTCCGTGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCTTGGGAAGACGGCGAGGGCAGCACCTGGACCTATGGACAGTGC
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCCTCCAGCATGTGGCACCTCTGTG
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGCAGCATGAGGTCCACGG
CATGCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTACCGATGAACTCTGAGTGTGGATGGATGGGTGGAGG
GTGGCAGGTGGGGCGTCTGCAGGCCACTCTTGGCAGAGACTTTGGTTGTAGGGTCCTC
AAGTGCCTTGTGATTAAAGAATGTTGGTCTATGAAA

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FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857  
><subunit 1 of 1, 221 aa, 1 stop  
><MW: 23598, pI: 6.96, NX(S/T): 0  
MWSAGRGAAWPVLLGLLLALLVPGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL  
SNNQEVSASFGEEDGEGLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCAGGCTGGTCTTGAAGTGCCTGACCTCCTAAAGTGTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACCTCATCTTCTTGATGAGATGAACACTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGGCTACCCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAACATGGTCCATTATGCCTTACAAACTTACACA
GTGCTTGGAAATTCAAAGTACTCAGTGGAGAGAGGTGTTCAGGAGCCGTAGAGCCAGAT
CGTCATATGTCTGCATTGTGGCTGCTGGCCTCCTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGATGCTATGAAACATCCAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTACGGCCTGAACACTGTGGAGTTCGTGTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTCTTGTCCAGGAAGTCTCCGGTGACAAAATTCTGGTC
AACATGGCGATAGGACTAGCATGGTCAGGACCCCTGGCTCTCAAGCTCCACATCCTGGAT
TAGTGAGTCTCAGGTTCCCAGACAACCTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCCTACAGTGGG
GGTGTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCCTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTCTTAACATCTCAGATGAAACCCAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAAACTAGCCAAGGGCACCTGTAACGGAAAT
CTGAGTTGACCTAAAGTCATTAAAATAACATGAATCCCATTAAAAAAAAAAAAAA

FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867  
><subunit 1 of 1, 194 aa, 1 stop  
><MW: 21431, pI: 8.57, NX(S/T): 0  
MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE  
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF
```

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTACAGCTGCTGGTGCACCATTCAGGACCCTGCC**ATGAAAG**
CCCTTATGCTGCTCACCCGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTAC
TCCTGCTACAAGGTCCCTGTGCTGGCTGTGTGGACCGGCAGTCCTGCCGCCGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATAACCTTGGTAAGATGTGGTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAAACACCACCTGCTGCAACAAGGACAAC TGCAACAGCGCAGGACCCCCGGCCCAC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTGGCTGGCCTGGCCTGGCTGCTGCAC**TGA**
ACTCATTCCATTGGCTGCCCTCCTCCCACCTGCCCTGGCCTGAGCCTCTCCCTGTGTCT
CTGTATCCCCTGGCTTACAGAATCGTCTCTCCCTAGCTCCATTCTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTCCCACCTCACACCCCTCACTCTCCTTTCTGGGT
CCCTTCCACTTCCTCCAGGACCTCATTGGCTCTAGAAGGGCTCCCCACTTGCTTCCT
ATACTCTGCTGTCCTACTTGAGGAGGGATTGGGATCTGGCCTGAAATGGGCTCTGTG
TTGTCCCCAGTGAAGGCTCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCCAGGCTCCATATGTACCCATCCCCATACTCACCTTTCCATTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAA

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FIGURE 44

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878  
><subunit 1 of 1, 125 aa, 1 stop  
><MW: 13821, pI: 8.60, NX(S/T): 2  
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN  
LRCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH
```

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGGCTGCAGCTCTGCA
GTCGGGCCGTTCTCGCCGCCGCCAGGGTAGCGGTGTAGCTGCAGCGTCGCCGCCT
ACCGCACCCAGGTTCGGCCGTAGGCCTGGCAGCCCCGGCCATCTCATCGAGCGCC**AT**
GGCCGCAGCCTGCGGGCCGGAGCGGCCGGTACTGCTGCTCCTCGGTTGCATTGTTTC
TGCTGACCAGCGGGCCCTGCCCTGGCTGGAACGACCCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCCTCCACTATGACCGCTATAACCACCTCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTACCCCCAAAAGTCATACAGTGTG
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTGGAAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTAGATTATACAGAACTTGGCCTGCAGAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTGCCTCTTGATTCTGATTATTATAAGTGGTCC
TCGGCGGATTCCGTAAACATGAGTGGATTGATTACCATCGTGGTACTCCTGGATGCCCT
TGTAGTCTATAAGCTGTTCTGAGTGACGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTCCCACCGTTACCAAGAGATTACCAACTCAGCAGGACCTCCTCCCCCAGGCTT
AAGTCTGAGTCACAGGACCACAGAATACTGCCATGGTGCACCTCTGGTTGGCAGTGC
TTTACAGGACAACAAGGATATGAAAATTCAAGGACCAGGGTTCTGGACAGGCTTGGAACTG
GTGGAATACTAGGATATTGTTGGCAGCAATAGAGCGGAAACACCCCTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTACCCCTGGCACGTGGAAATAGGGCTTACTCACCCCTCA
TGGAGGCTGGCAGCTATTGGTATGTTCAAACACTGACACAGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCACACTGGATGCAGAAAT
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GGGATATTCAAAAGTTCTGTTGTTATGCCAGTGTAGCTTTGTATTCTATTATTGAG
GCTAAAAGTTGATGTGACAAAATACTTATGTGTTATGTCAGTGTAAACATGCAGATGTA
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CTGTGATGCCCTAAGAACATTAAGAACATGAAAGGTGTTGACTAATAGAAACTAAGTACAGAA
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GAGATGGCCTCTGGTAAGTGAATATTACCTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTTGTTGAGCTGCTGGCAAAATGCTGAAACCTCTATATTCTTCT
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FIGURE 46

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889  
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VLRGSCGLEYNLDYTELGLQKLKESGKQHGFASFSDYYYKWSSADSCNMSGLITIVVLLGIA  
FVVYKLFSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFDSDWYPSYPPSYPGTWNRAYSP  
HGGSGSYSVCSNSDTKRTASGYGGTRRR
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318